



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/764,330

DATE: 08/20/2004

TIME: 10:46:02

Input Set : A:\SEQ.Listing.ST25.txt.txt

Output Set: N:\CRF4\08202004\J764330.raw

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3 <110> APPLICANT: Cooke, Michael P.
 4 Sauer, Karsten
 5 Wiltshire, Tim
 6 Tarantino, Lisa
 7 Fletcher, Colin
 8 Wen, Ben
 10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES
 12 <130> FILE REFERENCE: P1097US10
 14 <140> CURRENT APPLICATION NUMBER: US 10/764,330
 15 <141> CURRENT FILING DATE: 2004-01-23
 17 <150> PRIOR APPLICATION NUMBER: US 60/442,792
 18 <151> PRIOR FILING DATE: 2003-01-25
 20 <160> NUMBER OF SEQ ID NOS: 4
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1192
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Mus musculus
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 39 Phe Ala Leu Cys Pro Pro Pro Arg Pro Cys Cys Ser Ile Ser Ala Gln
 40 35 40 45
 43 Ser Tyr Gly Arg Arg Ala Ser Gly Thr Lys Pro Arg Ala Ala Gly Gly
 44 50 55 60
 47 Gly Gly Ala Gly Gly Gly Ala Gly Arg Arg Ala Ala Ala Gly Gly
 48 65 70 75 80
 51 Pro Cys Thr Met Ala Val Tyr Cys Tyr Ala Leu Asn Ser Leu Val Ile
 52 85 90 95
 55 Met Asn Ser Thr Asn Glu Leu Lys Ser Gly Gly Pro Arg Pro Ser Gly
 56 100 105 110
 59 Ser Glu Thr Pro Gln Pro Ser Gly Arg Ala Ala Leu Ser Pro Gly Ser
 60 115 120 125
 63 Val Phe Ser Pro Gly Arg Gly Ala Ser Phe Leu Phe Pro Pro Ala Glu
 64 130 135 140
 67 Ser Leu Ser Leu Glu Glu Pro Gly Ser Pro Gly Gly Trp Arg Ser Gly
 68 145 150 155 160
 71 Arg Arg Arg Leu Asn Ser Ser Ser Gly Ser Gly Gly Gly Ser Ser Ser
 72 165 170 175
 75 Ser Asn Ser Ser Ser Ser Gly Val Gly Ser Pro Ser Trp Ala Gly
 76 180 185 190

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79 Arg Leu Arg Gly Asp Ala Gln Gln Val Val Ala Ala Arg Ile Leu Ser
80      195      200      205
83 Pro Pro Gly Pro Glu Glu Ala Gln Arg Lys Leu Arg Ile Leu Gln Arg
84      210      215      220
87 Glu Leu Gln Asn Val Gln Val Asn Gln Lys Val Gly Met Phe Glu Ala
88 225      230      235      240
91 Gln Ile Gln Ala Gln Ser Ser Ala Ile Gln Ala Pro Arg Ser Pro Arg
92      245      250      255
95 Leu Gly Arg Ala Arg Ser Pro Ser Pro Cys Pro Phe Arg Ser Ser Ser
96      260      265      270
99 Gln Pro Pro Glu Arg Val Leu Ala Pro Cys Ser Pro Ser Glu Glu Arg
100     275     280     285
103 Arg Thr Lys Ser Trp Gly Glu Gln Cys Thr Glu Thr Pro Asp Thr Asn
104     290     295     300
107 Ser Gly Arg Arg Ser Arg Leu Ser Thr His Pro Ser Lys Asp Lys Glu
108 305     310     315     320
111 Gly Val Ala Pro Leu Leu Gly Pro Ala Ser Pro Thr Arg Leu Gly Thr
112     325     330     335
115 Gln Ser Pro Ser Thr Ser Val Arg Met Glu Arg Gly Thr Pro Ala Ser
116     340     345     350
119 Pro Arg Cys Gly Ser Pro Thr Pro Met Glu Thr Asp Lys Arg Val Ala
120     355     360     365
123 Pro Ser Leu Glu Arg Phe Gly Thr Ser Leu Thr Leu Ala Thr Lys Val
124     370     375     380
127 Ala Ala Ser Ala Ala Ser Ala Gly Pro His Pro Gly His Asp Ser Ala
128 385     390     395     400
131 Leu Met Glu Thr Gly Cys Glu Leu Gly Gly Met Arg Pro Trp Glu Ala
132     405     410     415
135 Gln Met Glu Arg Arg Gly Gln Phe Leu Gly Lys Glu Thr Gly Ser Thr
136     420     425     430
139 Pro Glu Pro Val Arg Thr His Met Arg Glu Pro Pro Gly Arg Val Gly
140     435     440     445
143 Arg Gly Ile His Ser Val Gly Gly Gln Gly Ser Trp Thr Pro Glu Val
144     450     455     460
147 Ile Lys Arg Pro Glu Glu Arg Ala Val Thr Ala Gln Ser Ser Glu Pro
148 465     470     475     480
151 Ser Glu Asp Pro Arg Trp Ser Arg Leu Pro Val Asp Leu Asp Ser Val
152     485     490     495
155 Gly Pro Glu Lys Gly Gly Asn Arg Ile Pro Gly Met Arg Gly Pro Gln
156     500     505     510
159 Gln Thr Leu Asp Ser Glu Arg Glu Gly Ser Pro Ala Leu Gly Leu Leu
160     515     520     525
163 Gly Gly Ser Gln Ala Ala Gln Pro Gly Ala Arg Gly Val Glu Glu Asp
164     530     535     540
167 Val His Tyr Gly Arg Met Leu Glu Pro Leu Pro Pro Gly Glu Val Thr
168 545     550     555     560
171 Thr Lys Leu Lys Glu Pro Gln Cys Leu Pro Gly Asp Arg Met Gly Met
172     565     570     575
175 Gln Pro Glu Ser Ser Ile Val Trp Pro Ser Ala Leu Glu Glu Ala Pro

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176          580          585          590
179 Leu Ile Trp Thr Arg Asp Thr Gly Val Gln Ser Lys Gly Thr Trp Gly
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183 Ser Gln Leu Pro Asp Gly Asp Ala His Pro Ser Cys Gln Glu Met Pro
184          610          615          620
187 Pro Asp Gln Lys Asp Lys Ala Ser Leu Lys Glu Ala Cys Ser Pro Ser
188 625          630          635          640
191 Asn Ile Pro Ala Ile Pro Ala Val Ile Ile Thr Asp Met Gly Ala Gln
192          645          650          655
195 Glu Asp Gly Gly Leu Glu Glu Ile Gln Gly Ser Pro Arg Gly Pro Leu
196          660          665          670
199 Pro Leu Arg Lys Leu Ser Ser Ser Ser Ala Ser Ser Thr Gly Phe Ser
200          675          680          685
203 Ser Ser Tyr Asp Asp Ser Glu Glu Asp Ile Ser Ser Asp Pro Glu Arg
204          690          695          700
207 Thr Leu Asp Pro Asn Ser Ala Phe Leu His Thr Leu Asp Gln Gln Lys
208 705          710          715          720
211 Pro Arg Val Ser Lys Ser Trp Arg Lys Ile Lys Asn Met Val Gln Trp
212          725          730          735
215 Ser Pro Phe Val Met Ser Phe Lys Lys Lys Tyr Pro Trp Ile Gln Leu
216          740          745          750
219 Ala Gly His Ala Gly Ser Phe Lys Ala Ala Ala Asn Gly Arg Ile Leu
220          755          760          765
223 Lys Lys His Cys Glu Ser Glu Gln Arg Cys Leu Asp Arg Leu Met Ala
224          770          775          780
227 Asp Val Leu Arg Pro Phe Val Pro Ala Tyr His Gly Asp Val Val Lys
228 785          790          795          800
231 Asp Gly Glu Arg Tyr Asn Gln Met Asp Asp Leu Leu Ala Asp Phe Asp
232          805          810          815
235 Ser Pro Cys Val Met Asp Cys Lys Met Gly Val Arg Thr Tyr Leu Glu
236          820          825          830
239 Glu Glu Leu Thr Lys Ala Arg Lys Lys Pro Ser Leu Arg Lys Asp Met
240          835          840          845
243 Tyr Gln Lys Met Val Glu Val Asp Pro Glu Ala Pro Thr Glu Glu Glu
244          850          855          860
247 Lys Ala Gln Arg Ala Val Thr Lys Pro Arg Tyr Met Gln Trp Arg Glu
248 865          870          875          880
251 Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys
252          885          890          895
255 Lys Glu Asp Gly Ser Val Asn Arg Asp Phe Lys Lys Thr Lys Thr Arg
256          900          905          910
259 Glu Gln Val Thr Glu Ala Phe Arg Glu Phe Thr Lys Gly Asn Gln Asn
260          915          920          925
263 Ile Leu Ile Ala Tyr Arg Asp Arg Leu Lys Ala Ile Arg Ala Thr Leu
264          930          935          940
267 Glu Ile Ser Pro Phe Phe Lys Cys His Glu Val Ile Gly Ser Ser Leu
268 945          950          955          960
271 Leu Phe Ile His Asp Lys Lys Glu Gln Ala Lys Val Trp Met Ile Asp
272          965          970          975

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275 Phe Gly Lys Thr Thr Pro Leu Pro Glu Gly Gln Thr Leu Gln His Asp
276          980          985          990
279 Val Pro Trp Gln Glu Gly Asn Arg Glu Asp Gly Tyr Leu Ser Gly Leu
280          995          1000          1005
283 Asp Asn Leu Ile Asp Ile Leu Thr Glu Met Ser Gln Gly Ser Pro
284          1010          1015          1020
287 Leu Thr Gly His Arg His Arg Ala Pro Cys His Phe Ala Arg His
288          1025          1030          1035
291 Leu Cys Leu Ser Pro Leu Ser Ser Pro Asn Ser Ser Phe Ser Cys
292          1040          1045          1050
295 Leu Ser Ala Tyr Leu Glu Gln Ser Leu Pro Ser Ala Leu Gln Asp
296          1055          1060          1065
299 Thr Leu Glu Lys Lys Lys Arg Phe Phe Phe Ser Arg Ser Leu Leu
300          1070          1075          1080
303 Pro Arg Pro Pro Thr Gly Leu Gly Gly Gly Val Ser His Ala Leu
304          1085          1090          1095
307 Ile Glu Pro Pro Ser Arg Arg Glu Leu His Lys Ala Arg Pro His
308          1100          1105          1110
311 Ile Leu Leu His Ser Glu Ser Ala Arg Val Gln Lys Ala Val Ser
312          1115          1120          1125
315 Leu Val Ala Ser Leu Glu Arg Leu Ser Leu Pro Leu Gly Asp Thr
316          1130          1135          1140
319 Ala Pro Leu Pro Glu Asn Ser Gly Pro His Trp Leu Pro Val Gly
320          1145          1150          1155
323 Ala Leu Leu Pro Pro Ser Gly Cys His Gln Ala Gln Ser His Leu
324          1160          1165          1170
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332          1190
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345 gtgctgagcc ccggcagcgt ttccagcccc gggagaggcg cctctttcct cttcccccca      180
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363 ggagggccca gcctatgctc ctgcaggtg aagaaaggaa tgccacctct tcccggccgg      720
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448 ctgagccccg gcagcgtctt cagccctggg agaggcgctt cctttctctt cccccagca 180
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VERIFICATION SUMMARY

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